

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

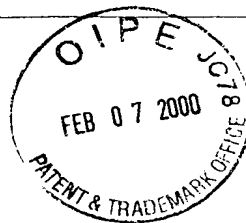
Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.

SEQUENCE LISTING



<110> Zuker, Charles S.  
Adler, Jon Elliot  
Lindemeier, Juergen  
Ryba, Nick  
Hoon, Mark  
The Regents of the University of California

<120> Nucleic Acids Encoding a G-Protein Coupled Receptor  
Involved in Sensory Transduction

<130> 02307E-088610US

<140> US 09/361,652

<141> 1999-07-27

<150> US 60/094,465

<151> 1998-07-28

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 840

<212> PRT

<213> Rattus sp.

<220>

<223> rat G-protein coupled receptor B3 (GPCR-B3)

<400> 1

Met Leu Phe Trp Ala Ala His Leu Leu Leu Ser Leu Gln Leu Val Tyr  
1 5 10 15

Cys Trp Ala Phe Ser Cys Gln Arg Thr Glu Ser Ser Pro Gly Phe Ser  
20 25 30

Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His Gly Asp  
35 40 45

Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp Arg Pro  
50 55 60

Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met Arg Phe  
65 70 75 80

Thr Val Glu Glu Ile Asn Asn Ser Ser Ala Leu Leu Pro Asn Ile Thr  
85 90 95

Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ala Asn Val Tyr  
100 105 110

Ala Thr Leu Arg Val Leu Ala Leu Gln Gly Pro Arg His Ile Glu Ile  
115 120 125

Gln Lys Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Phe Ile Gly  
130 135 140

Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu Gly Pro  
 145 150 155 160  
 Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Val Leu Ser  
 165 170 175  
 Ala Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Val Pro Ser Asp Arg  
 180 185 190  
 His Gln Val Glu Val Met Val Gln Leu Leu Gln Ser Phe Gly Trp Val  
 195 200 205  
 Trp Ile Ser Leu Ile Gly Ser Tyr Gly Asp Tyr Gly Gln Leu Gly Val  
 210 215 220  
 Gln Ala Leu Glu Glu Leu Ala Val Pro Arg Gly Ile Cys Val Ala Phe  
 225 230 235 240  
 Lys Asp Ile Val Pro Phe Ser Ala Arg Val Gly Asp Pro Arg Met Gln  
 245 250 255  
 Ser Met Met Gln His Leu Ala Gln Ala Arg Thr Thr Val Val Val Val  
 260 265 270  
 Phe Ser Asn Arg His Leu Ala Arg Val Phe Phe Arg Ser Val Val Leu  
 275 280 285  
 Ala Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Asp Trp Ala Ile  
 290 295 300  
 Ser Thr Tyr Ile Thr Ser Val Thr Gly Ile Gln Gly Ile Gly Thr Val  
 305 310 315 320  
 Leu Gly Val Ala Val Gln Gln Arg Gln Val Pro Gly Leu Lys Glu Phe  
 325 330 335  
 Glu Glu Ser Tyr Val Arg Ala Val Thr Ala Ala Pro Ser Ala Cys Pro  
 340 345 350  
 Glu Gly Ser Trp Cys Ser Thr Asn Gln Leu Cys Arg Glu Cys His Thr  
 355 360 365  
 Phe Thr Thr Arg Asn Met Pro Thr Leu Gly Ala Phe Ser Met Ser Ala  
 370 375 380  
 Ala Tyr Arg Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly Leu His  
 385 390 395 400  
 Gln Leu Leu Gly Cys Thr Ser Glu Ile Cys Ser Arg Gly Pro Val Tyr  
 405 410 415  
 Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu Leu His  
 420 425 430  
 Glu Asn Thr Val Ala Phe Asp Asp Asn Gly Asp Thr Leu Gly Tyr Tyr  
 435 440 445  
 Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe Glu Ile  
 450 455 460

Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn Lys Thr  
 465 470 475 480  
 Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser Val Cys  
 485 490 495  
 Thr Thr Asp Cys Leu Ala Gly His His Arg Val Val Val Gly Ser His  
 500 505 510  
 His Cys Cys Phe Glu Cys Val Pro Cys Glu Ala Gly Thr Phe Leu Asn  
 515 520 525  
 Met Ser Glu Leu His Ile Cys Gln Pro Cys Gly Thr Glu Glu Trp Ala  
 530 535 540  
 Pro Lys Glu Ser Thr Thr Cys Phe Pro Arg Thr Val Glu Phe Leu Ala  
 545 550 555 560  
 Trp His Glu Pro Ile Ser Leu Val Leu Ile Ala Ala Asn Thr Leu Leu  
 565 570 575  
 Leu Leu Leu Leu Val Gly Thr Ala Gly Leu Phe Ala Trp His Phe His  
 580 585 590  
 Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met Leu  
 595 600 605  
 Gly Ser Leu Val Ala Gly Ser Cys Ser Phe Tyr Ser Phe Phe Gly Glu  
 610 615 620  
 Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser Leu Gly  
 625 630 635 640  
 Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln Leu Val  
 645 650 655  
 Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr Arg Thr Trp  
 660 665 670  
 Ala Gln Asn His Gly Ala Gly Leu Phe Val Ile Val Ser Ser Thr Val  
 675 680 685  
 His Leu Leu Ile Cys Leu Thr Trp Leu Val Met Trp Thr Pro Arg Pro  
 690 695 700  
 Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu Cys Thr  
 705 710 715 720  
 Glu Val Asn Ser Val Gly Phe Leu Leu Ala Phe Thr His Asn Ile Leu  
 725 730 735  
 Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu Leu Pro  
 740 745 750  
 Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Leu Asn  
 755 760 765  
 Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ala Ser Ile Tyr Gln Gly  
 770 775 780

Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Thr Thr Leu Ser  
785 790 795 800

Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu Cys  
805 810 815

Arg Pro Glu Leu Asn Asn Thr Glu His Phe Gln Ala Ser Ile Gln Asp  
820 825 830

Tyr Thr Arg Arg Cys Gly Thr Thr  
835 840

<210> 2

<211> 842

<212> PRT

<213> Mus sp.

<220>

<223> mouse G-protein coupled receptor B3 (GPCR-B3)

<400> 2

Met Leu Phe Trp Ala Ala His Leu Leu Leu Ser Leu Gln Leu Ala Val  
1 5 10 15

Ala Tyr Cys Trp Ala Phe Ser Cys Gln Arg Thr Glu Ser Ser Pro Gly  
20 25 30

Phe Ser Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His  
35 40 45

Ala Asp Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp  
50 55 60

Arg Ser Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met  
65 70 75 80

Arg Phe Thr Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn  
85 90 95

Ile Thr Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ser Asn  
100 105 110

Val Tyr Ala Thr Leu Arg Val Pro Ala Gln Gln Gly Thr Gly His Leu  
115 120 125

Glu Met Gln Arg Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Leu  
130 135 140

Ile Gly Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu  
145 150 155 160

Ser Pro Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Ile  
165 170 175

Leu Ser Gly Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Ile Pro Ser  
180 185 190

Asp Lys Tyr Gln Val Glu Val Ile Val Arg Leu Leu Gln Ser Phe Gly  
195 200 205

Trp Val Trp Ile Ser Leu Val Gly Ser Tyr Gly Asp Tyr Gly Gln Leu  
 210 215 220  
 Gly Val Gln Ala Leu Glu Glu Leu Ala Thr Pro Arg Gly Ile Cys Val  
 225 230 235 240  
 Ala Phe Lys Asp Val Val Pro Leu Ser Ala Gln Ala Gly Asp Pro Arg  
 245 250 255  
 Met Gln Arg Met Met Leu Arg Leu Ala Arg Ala Arg Thr Thr Val Val  
 260 265 270  
 Val Val Phe Ser Asn Arg His Leu Ala Gly Val Phe Phe Arg Ser Val  
 275 280 285  
 Val Leu Ala Asn Leu Thr Gly Lys Val Trp Ile Ala Ser Glu Asp Trp  
 290 295 300  
 Ala Ile Ser Thr Tyr Ile Thr Asn Val Pro Gly Ile Gln Gly Ile Gly  
 305 310 315 320  
 Thr Val Leu Gly Val Ala Ile Gln Gln Arg Gln Val Pro Gly Leu Lys  
 325 330 335  
 Glu Phe Glu Glu Ser Tyr Val Gln Ala Val Met Gly Ala Pro Arg Thr  
 340 345 350  
 Cys Pro Glu Gly Ser Trp Cys Gly Thr Asn Gln Leu Cys Arg Glu Cys  
 355 360 365  
 His Ala Phe Thr Thr Trp Asn Met Pro Glu Leu Gly Ala Phe Ser Met  
 370 375 380  
 Ser Ala Ala Tyr Asn Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly  
 385 390 395 400  
 Leu His Gln Leu Leu Gly Cys Thr Ser Gly Thr Cys Ala Arg Gly Pro  
 405 410 415  
 Val Tyr Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu  
 420 425 430  
 Leu His Lys Lys Thr Val Ala Phe Asp Asp Lys Gly Asp Pro Leu Gly  
 435 440 445  
 Tyr Tyr Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe  
 450 455 460  
 Glu Val Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn  
 465 470 475 480  
 Lys Thr Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser  
 485 490 495  
 Val Cys Thr Arg Asp Cys Leu Glu Gly His His Arg Leu Val Met Gly  
 500 505 510  
 Ser His His Cys Cys Phe Glu Cys Met Pro Cys Glu Ala Gly Thr Phe  
 515 520 525

Leu Asn Thr Ser Glu Leu His Thr Cys Gln Pro Cys Gly Thr Glu Glu  
 530 535 540  
 Trp Ala Pro Glu Gly Ser Ser Ala Cys Phe Ser Arg Thr Val Glu Phe  
 545 550 555 560  
 Leu Gly Trp His Glu Pro Ile Ser Leu Val Leu Leu Ala Ala Asn Thr  
 565 570 575  
 Leu Leu Leu Leu Leu Leu Ile Gly Thr Ala Gly Leu Phe Ala Trp Arg  
 580 585 590  
 Leu His Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu  
 595 600 605  
 Met Leu Gly Ser Leu Val Ala Gly Ser Cys Ser Leu Tyr Ser Phe Phe  
 610 615 620  
 Gly Lys Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser  
 625 630 635 640  
 Leu Gly Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln  
 645 650 655  
 Leu Val Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His  
 660 665 670  
 Thr Trp Ala Gln Asn His Gly Ala Gly Ile Phe Val Ile Val Ser Ser  
 675 680 685  
 Thr Val His Leu Phe Leu Cys Leu Thr Trp Leu Ala Met Trp Thr Pro  
 690 695 700  
 Arg Pro Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu  
 705 710 715 720  
 Cys Thr Glu Val Asn Ser Val Gly Phe Leu Val Ala Phe Ala His Asn  
 725 730 735  
 Ile Leu Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu  
 740 745 750  
 Leu Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu  
 755 760 765  
 Leu His Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ser Ser Ile Tyr  
 770 775 780  
 Gln Gly Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Ala Thr  
 785 790 795 800  
 Leu Ser Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile  
 805 810 815  
 Leu Cys Arg Pro Glu Leu Asn Asn Thr Glu His Phe Gln Ala Ser Ile  
 820 825 830  
 Gln Asp Tyr Thr Arg Arg Cys Gly Thr Thr  
 835 840

<210> 3  
 <211> 777  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human G-protein coupled receptor B3 (GPCR-B3)

<400> 3  
 Arg Ser Cys Ser Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met  
 1 5 10 15  
 Arg Leu Gly Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn  
 20 25 30  
 Ile Thr Leu Gly Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn  
 35 40 45  
 Val Tyr Ala Thr Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile  
 50 55 60  
 Glu Leu Gln Gly Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val  
 65 70 75 80  
 Ile Gly Pro Asp Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu  
 85 90 95  
 Ser Pro Phe Leu Val His Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu  
 100 105 110  
 Ser Val Lys Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp  
 115 120 125  
 Lys Tyr Gln Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp  
 130 135 140  
 Thr Trp Ile Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln Leu Gly  
 145 150 155 160  
 Val Gln Ala Leu Glu Asn Gln Ala Leu Val Arg Gly Ile Cys Ile Ala  
 165 170 175  
 Phe Lys Asp Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met  
 180 185 190  
 Gln Cys Leu Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val Val  
 195 200 205  
 Val Phe Ser Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val  
 210 215 220  
 Leu Thr Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala  
 225 230 235 240  
 Leu Ser Arg His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met  
 245 250 255  
 Val Leu Gly Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Lys Ala  
 260 265 270



Phe Glu Glu Ala Tyr Ala Arg Ala Asp Lys Glu Ala Pro Arg Pro Cys  
 275 280 285  
 His Lys Gly Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln  
 290 295 300  
 Ala Phe Met Ala His Thr Met Pro Lys Leu Lys Ala Phe Ser Met Ser  
 305 310 315 320  
 Ser Ala Tyr Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu  
 325 330 335  
 His Gln Leu Leu Gly Cys Ala Ser Glu Leu Cys Ser Arg Gly Arg Val  
 340 345 350  
 Tyr Pro Trp Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu  
 355 360 365  
 His Lys Asp Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser  
 370 375 380  
 Tyr Asn Ile Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr  
 385 390 395 400  
 Val Leu Gly Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu  
 405 410 415  
 Thr Lys Ile Gln Trp His Gly Lys Asn His Gln Val Pro Lys Ser Val  
 420 425 430  
 Cys Ser Ser Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe  
 435 440 445  
 His His Cys Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu  
 450 455 460  
 Asn Lys Ser Glu Leu Tyr Arg Cys Gln Pro Cys Gly Thr Glu Glu Trp  
 465 470 475 480  
 Ala Pro Glu Gly Ser Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu  
 485 490 495  
 Ala Leu Arg Glu His Thr Ser Trp Val Leu Leu Ala Ala Asn Thr Leu  
 500 505 510  
 Leu Leu Leu Leu Leu Leu Gly Thr Ala Gly Leu Phe Ala Trp His Leu  
 515 520 525  
 Asp Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met  
 530 535 540  
 Leu Gly Ser Leu Ala Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly  
 545 550 555 560  
 Glu Pro Thr Arg Pro Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu  
 565 570 575  
 Gly Phe Thr Ile Phe Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu  
 580 585 590

Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala  
 595 600 605  
 Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala  
 610 615 620  
 Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu  
 625 630 635 640  
 Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys  
 645 650 655  
 Thr Glu Thr Asn Ser Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly  
 660 665 670  
 Leu Leu Ser Ile Ser Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu  
 675 680 685  
 Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Phe  
 690 695 700  
 Asn Phe Val Ser Trp Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Asp  
 705 710 715 720  
 Gly Lys Tyr Leu Pro Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu  
 725 730 735  
 Ser Ser Gly Phe Gly Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu  
 740 745 750  
 Cys Arg Pro Asp Leu Asn Ser Thr Glu His Phe Gln Ala Ser Ile Gln  
 755 760 765  
 Asp Tyr Thr Arg Arg Cys Gly Ser Thr  
 770 775

<210> 4  
 <211> 2771  
 <212> DNA  
 <213> Rattus sp.

<220>  
 <223> rat G-protein coupled receptor B3 (GPCR-B3)

<400> 4  
 attcacatca gagctgtgct cagccatgct gggcagaggg acgacggctg gccagcatgc 60  
 tcttctgggc tgctcacctg ctgctcagcc tgcagttggt ctactgctgg gctttcagct 120  
 gccaaaggac agagtccctc ccaggettca gccttcctgg ggacttcctc cttgcaggtc 180  
 tgttctccct ccatggtgac tgtctgcagg tgagacacag acctctggtg acaagttgtg 240  
 acaggcccga cagcttcaac ggccatggct accacctctt ccaagccatg cggttcactg 300  
 ttgaggagat aaacaactcc tcggccctgc ttccaacat caccctgggg tatgagctgt 360  
 acgacgtgtg ctccagaatct gccaatgtgt atgccaccct gaggggtgctt gccctgcaag 420  
 ggccccgcca catagagata cagaaagacc ttcgcaacca ctccctccaag gtggtggcct 480  
 tcatcgggcc tgacaacact gaccacgctg tcaactaccgc tgcccttgctg ggtcccttcc 540  
 tgatgcccct ggtcagctat gaggcaagca gcgtggtact cagtgccaaag cgcaagttcc 600  
 cgtctttcct tcgtaccgtc cccagtgacc ggcaccaggt ggaggtcatg gtgcagctgc 660  
 tgcagagttt tgggtgggtg tggatctcgc tcattggcag ctacggtgat tacgggcagc 720  
 tgggtgtgca ggcgctggag gagctggcgc tgccccgggg catctgcgtc gccttcaagg 780  
 acatcggtgcc tttctctgcc cgggtgggtg acccgaggat gcagagcatg atgcagcatc 840  
 tggctcaggc caggaccacc gtggttgtg tcttctctaa ccggcacctg gctagagtgt 900

tcttcaggctc cgtgggtgctg gccaacctga ctggcacaagt gtgggtcgcc tcagaagact 960  
gggccatctc cacgtacatc accagcgtga ctgggatcca aggcattggg acgggtgctcg 1020  
gtgtggccgt ccagcagaga caagtcacctg ggctgaagga gtttgaggag tcttatgtca 1080  
gggctgtaac agctgctccc agcgtttgcc cggaggggtc ctggtgcagc actaaccagc 1140  
tgtgccggga gtgccacacg ttcaagactc gtaacatgcc cagccttggg gccttctcca 1200  
tgagtggcgc ctacagagtg tatgaggctg tgtacgctgt ggcccacggc ctccaccagc 1260  
tcctgggatg tacttctgag atctgttcca gagggccagt ctaccctggg cagcttcttc 1320  
agcagatcta caaggtgaat tttcttctac atgagaatac tgtggcattt gatgacaacg 1380  
gggacactct aggttactac gacatcatcg cctgggactg gaatggacct gaatggacct 1440  
ttgagatcat tggctctgcc tcaactgtctc cagttcatct ggacataaat aagacaaaaa 1500  
tccagtggca cgggaagaac aatcagggtg ctgtgtcagt gtgtaccacg gactgtctgg 1560  
cagggcacca caggggtggt gtgggttccc accactgctg ctttgagtgt gtgccctgcg 1620  
aagctgggac ctttctcaac atgagtgage ttacatctg ccagccttgt ggaacagaag 1680  
aatgggcacc caaggagagc actacttget tcccacgcac ggtggagttc ttggcttggc 1740  
atgaacccat ctctttgggt ctaatagcag ctaacacgct attgctgctg ctgctggttg 1800  
ggactgctgg cctgtttgcc tggcattttc acacacctgt agtgaggta gctgggggta 1860  
ggctgtgctt cctcatgctg ggttccctgg tggccggaag ttgcagcttc tatagcttct 1920  
tcggggagcc caggtgccc gcgtgcttgc tgcgtcagcc cctcttttct ctggggttg 1980  
ccatcttctt ctctgctg acaatcgcgt ccttccaaact ggtcatcatc ttcaagtttt 2040  
ctaccaaggt gccacatct taccgtacct ggcccaaaaa ccatggtgca ggtctattcg 2100  
tcattgtcag ctccacggtc catttgctca tctgtctcac atggcttgta atgtggacct 2160  
cacgaccac caggaatac cagcgttcc ccatctggt gattctcgag tgcacagagg 2220  
tcaactctgt aggttctctg ttggctttca cccacaacat tctcctctcc atcagtacct 2280  
tcgtctgcag ctacctgggt aaggaaactg cagagaacta taatgaagcc aaatgtgtca 2340  
ccttcagcct gctcctcaac ttctgtacct ggatcgctt cttcaccatg gccagcattt 2400  
accagggcag ctacctgctt gcggtcaatg tgctggcagg gctgaccaca ctgagcggcg 2460  
gcttcagcgg ttacttctc cccaagtget atgtgattct ctgccgtcca gaactcaaca 2520  
atacagaaca ctttcaggcc tccatccagg actacacgag gcgctgcggc actacctgat 2580  
ccactggaaa ggtgcagacg ggaagggaag ctctcttctt gtgctgaagg tggcgggtcc 2640  
agtggggccg agagcttgag gtgtctggga gagctccggc acagcttacg atgtataagc 2700  
acgcggaaga atccagtgc ataaagacgg gaagtgtgaa aaaaaaaaaa aaaaaaaaaa 2760  
aaaaaaaaa a 2771

<210> 5  
<211> 2579  
<212> DNA  
<213> Mus sp.

<220>  
<223> mouse G-protein coupled receptor B3 (GPCR-B3)

<400> 5  
tttggccagc atgcttttct gggcagctca cctgctgctc agcctgcagc tggccggttg 60  
ttactgctgg gctttcagct gccaaaggac agaatcctct ccaggtttca gcctccctgg 120  
ggacttcttc ctggcaggcc tgttctccct ccatgctgac tgtctgcagg tgagacacag 180  
acctctgggt acaagtgtg acaggtctga cagcttcaac ggccatggct atcacctctt 240  
ccaagccatg cggttcaccg ttgaggagat aaacaactcc acagctctgc ttcccaacat 300  
caccctgggg tatgaactgt atgacgtgtg ctacagagtct tccaatgtct atgccacct 360  
gaggggtgccc gccagcaag ggacaggcca cctagagatg cagagagatc ttcgcaacca 420  
ctcctccaag gtggtggcac tcattgggccc tgataaacact gaccacgctg tcaccactgc 480  
tgccctgctg agcccttttc tgatgcccct ggtcagctat gaggcgagca gcgtgatcct 540  
cagtgggaag cgcaagtctc cgtccttctt gcgcaccatc cccagcgata agtaccaggt 600  
ggaagtcata gtgcggctgc tgcagagctt cggttgggtc tggatctcgc tcgttggcag 660  
ctatggtgac tacgggcagc tgggcgtaca ggcgtggag gagctggcca ctccacgggg 720  
catctgcgtc gcttcaagg acgtggtgcc tctctccgcc caggcgggtg acccaaggat 780  
gcagcgcagt atgctgcgtc tggctcgagc caggaccacc gtggtcgtgg tcttctctaa 840  
ccggcacctg gctggagtgt tcttcaggtc tgtggtgctg gccaacctga ctggcaaaagt 900  
gtggatcgcc tccgaagact gggccatctc cacgtacatc accaatgtgc ccgggatcca 960  
gggcattggg acggtgctgg ggggtggccat ccagcagaga caagtcacct gcctgaagga 1020  
gtttgaagag tcctatgtcc aggcagtgat ggggtgctccc agaacttgcc cagaggggtc 1080

ctggtgcggc actaaccage tgtgcaggga gtgtcacgct ttcacgacat ggaacatgcc 1140  
 cgagcttgga gccttctcca tgagcgctgc ctacaatgtg tatgaggctg tgtatgctgt 1200  
 ggcccacggc ctccaccage tcttgggatg tacctctggg acctgtgcca gaggcccagt 1260  
 ctacccttgg cagcttcttc agcagatcta caaggatgaat ttccttctac ataagaagac 1320  
 tgtagcattc gatgacaagg gggaccctct aggttattat gacatcatcg cctgggactg 1380  
 gaatggacct gaatggacct ttgaggatcat tggttctgcc tcaactgtctc cagttcatct 1440  
 agacataaat aagacaaaaa tccagtggca cgggaagaac aatcagggtgc ctgtgtcagt 1500  
 gtgtaccagg gactgtctcg aagggcacca caggttggtc atgggttccc accactgctg 1560  
 cttcgagtgc atgccctgtg aagctgggac atttctcaac acgagtgagc ttcacacctg 1620  
 ccagccttgt ggaacagaag aatgggcccc tgaggggagc tcagcctgct tctcacgcac 1680  
 cgtggagttc ttgggggtggc atgaacccat ctctttgtgt ctattagcag ctaacacgct 1740  
 attgctgctg ctgctgattg ggactgctgg cctgtttgcc tggcgtcttc acacgcctgt 1800  
 tgtgaggtca gctgggggta ggctgtgctt cctcatgctg ggttccttgg tagctgggag 1860  
 ttgcagcctc tacagcttct tcgggaagcc caccgtgccc gcgtgcttgc tgcgtcagcc 1920  
 cctcttttct ctcggttttg ccattttctt ctctgtctg acaatccgct ccttccaaact 1980  
 ggatcatcat tccaagtttt ctaccaaggt acccacattc taccacactt gggcccaaaa 2040  
 ccattggtgc ggaatattcg tcattgtcag ctccacggtc catttgttcc tctgtctcac 2100  
 gtggccttga atgtggacct cacggcccac caggagtag cagcgttccc cccatctggt 2160  
 gattcttgag tgcacagagg tcaactctgt gggcttctct gtggccttcg cacacaacat 2220  
 cctcctctcc atcagcacct ttgtctgcag ctacctgggt aaggaaactgc cggagaacta 2280  
 taacgaagcc aaatgtgtca ccttcagcct gctcctccac ttcgtatcct ggatcgcttt 2340  
 cttcaccatg tccagcattt accagggcag ctacctacc gcggtcaatg tgctggcagg 2400  
 gctggccact ctgagtggcg gcttcagcgg ctatttctc cctaaatgct acgtgattct 2460  
 ctgccgtcca gaactcaaca acacagaaca ctttcaggcc tccatccagg actacacgag 2520  
 gcgctgcggc actacctgag gcgctgcggc actacctgag gcgctgcggc actacctga 2579

<210> 6

<211> 2333

<212> DNA

<213> Homo sapiens

<220>

<223> human G-protein coupled receptor (GPCR-B3)

<400> 6

aggtcttgta gcttcaatga gcatggctac cacctcttcc aggctatgag gcttgggggtt 60  
 gaggagataa acaactccac ggccctgctg cccaacatca ccctggggta ccagctgtat 120  
 gatgtgtgtt ctgactctgc caatgtgtat gccacgctga gagtgcctc cctgccaggg 180  
 caacaccaca tagagctcca aggagacct ctccactatt cccctacggt gctggcagtg 240  
 attgggcctg acagcaccaa ccgtgctgcc accacagccg ccctgctgag ccttttctct 300  
 gtgcataatta gctatgcggc cagcagcgag acgctcagcg tgaagcggca gtatccctct 360  
 ttctgcgca ccatcccca tgacaagtac cagggtggaga ccatggtgct gctgctgcag 420  
 aagttcgggt ggacctggat ctctctgggt ggcagcagtg acgactatgg gcagctaggg 480  
 gtgcaggcac tggagaacca ggccctggtc aggggcatct gcattgcttt caaggacatc 540  
 atgcccttct ctgcccagggt gggcgatgag aggatgcagt gcctcatgag ccacctggcc 600  
 caggccgggg ccaccgtcgt ggttgttttt tccagccggc agttggccag ggtgtttttc 660  
 gagtccgtgg tgctgaccaa cctgactggc aaggtgtggg tcgcctcaga agcctggggc 720  
 ctctccaggc acatcactgg ggtgcccggg atccagcgca ttgggatggg gctgggcgtg 780  
 gccatccaga agagggctgt ccctggcctg aaggcgcttg aagaagccta tgcccgggca 840  
 gacaaggagg cccctaggcc ttgcacaagg gctcctgggt cagcagcaat cagctctgca 900  
 gagaatgccag agctttcatg gcacacacga tgcccaagct caaagccttc tccatgagtt 960  
 ctgcctacaa cgcataccgg gctgtgtatg cgggtggcca tggcctccac cagctcctgg 1020  
 gctgtgcctc tgagctctgt tccaggggccc gagtctatccc ctggcagctt ttggagcaga 1080  
 tccacaagggt gcatttctct ctacacaagg aactgtggc gtttaatgac aacagagatc 1140  
 ccctcagtag ctataacata attgcctggg actggaatgg acccaagtgg accttcacgg 1200  
 tctcgggttc ctccaatgg tctccagttc agctaaacat aaatgagacc aaaatccagg 1260  
 ggcacggaaa gaaccaccag gtgcctaagt ctgtgtgttc cagcagactgt cttgaagggc 1320  
 accagcgagt gggtacgggt ttccatcact gctgctttga gtgtgtgccc tgtggggctg 1380  
 ggaccttctt caacaagagc gagctctaca gatgccagcc ttgtggaaca gaagagtggg 1440  
 cacctgaggg aagccagacc tgcttcccgc gcactgtggg gtttttggct ttgcgtgagc 1500

acacctcttg ggtgctgctg gcagctaaca cgctgctgct gctgctgctg cttgggactg 1560  
 ctggcctggt tgccctggcac cttagacaccc ctgtggtgag gtcagcaggg ggccgcctgt 1620  
 gctttcttat gctgggctcc ctggcagcag gtagtggcag cctctatggc ttctttgggg 1680  
 aaccacaaag gcctgcgtgc ttgctaagcc aggcctctt tgcccttggt ttcaccatct 1740  
 tcctgtcctg cctgacagtt cgctcattcc aactaatcat catcttcaag ttttccacca 1800  
 aggtacctac attctaccac gcctgggtcc aaaaccacgg tgctggcctg tttgtgatga 1860  
 tcagctcagc ggcccagctg cttatctgtc taacttggct ggtggtgtgg accccactgc 1920  
 ctgctaggga ataccagcgc ttccccatc tggatgctg tgagtgcaca gagaccaact 1980  
 ccctgggctt catactggcc ttctcttaca atggcctcct ctccatcagt gcctttgcct 2040  
 gcagctacct gggtaaggac ttgccagaga actacaacga ggccaaatgt gtcaccttca 2100  
 gcctgctctt caacttcgtg tcttgatcg ccttcttcac cacggccagc gtctacgacg 2160  
 gcaagtacct gcctgcggcc aacatgatgg ctgggctgag cagcctgagc agcggcttcg 2220  
 gtgggtatct tctgcctaag tgctacgtga tctctgccc cccagacctc aacagcacag 2280  
 agcacttcca ggcctccatt caggactaca cgaggcgctg cggctccacc tga 2333

<210> 7  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:amino acid  
 sequence encoded by degenerate primer

<400> 7  
 Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp  
 1 5 10

<210> 8  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:amino acid  
 sequence encoded by degenerate primer

<400> 8  
 Leu Pro Glu Asn Tyr Asn Glu Ala Lys Cys  
 1 5 10



Application No.: 09/361,652

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**